

FIGURE 1

CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAAATATTTTAAATATT
AATATACATTTCTTCTGTGTCAGAAATACATAAACTTTATTATATCAGCGCAGG
5 GCGGCGCGGCGTCCGTCGCGGAGCAGAACCCGGCTTTTCTTGGAGCGACG
CTGTCTCTAGTCGCTGATCCCAATGCACCGGCTCATCTTTGTCTACACTCTA
ATCTGCGCAAACTTTTCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCG
CATCCATCAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG
10 CTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTG
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTGACA
ATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATCTGTAGGTATGATTTTGT
GGAAGTTGAAGATATATCCGAAACCACTACCATTTAGAGGACGATGGTGT
GGACACAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAACCAATTA
15 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTA
TTATCTTTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGG
AATCTGTCACAAGCTCTATTTCAAGGGTATCCTATAACTCTCCATCAGTAACG
GATCCCCTCTGATTGCGGATGCTCTGGACAAAAAATTGCAGAAATTGATA
CAGTGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT
20 TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTATACCATGAC
CGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA
GTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGC
CAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATT
GTGGCTGTGGAAGTGTCAACTGGAGGTCTGACATGCAATTCAGGAAAAAC
25 CGTGA AAAAGTATCATGAGGTATTACAGTTTGAGCTGGCCACATCAAGAGG
AGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATG
AACGATGTGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTGAGATAAG
AGACCCCTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCAATGAA
30 CACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGA
AAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAATA

FIGURE 2

1 CTA AAAAATATGTTCTCTACAACACCAAGGCTCATTA AAAATATTT
 46 TAAATATTAATATACATTTCTTCTGTGCAGAAATACATAAACTTT
 5 91 ATTATATCAGCGCAGGGCGGCGCGGCTCGGTCCCGGAGCAGAA
 136 CCCGGCTTTTCTTGGAGCGACGCTGTCTCTAGTCGCTGATCCCA

181 AATGCACCGGCTCATCTTTGTCTACACTCTAATCTGCGCAAATTT
 MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe
 10 226 TTGCAGCTGTCTGGGACACTTCTGCAACCCCGCAGAGCGCATCCAT
 CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle

271 CAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
 15 LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis

316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG
 LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly

361 AAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGTACCCACG
 20 AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg

406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAATACACG
 AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg
 25 451 GATACAGCTAGTGTTTGACAATCAGTTTGGATTAGAGGAAGCAGA
 IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu

496 AAATGATATCTGTAGGTATGATTTTTGTGGAAGTTGAAGATATATC
 30 AsnAspIleCysArgTyrAspPheValGluValGluAspIleSer

541 CGAAACCAAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGA
 GluThrSerThrIleIleArgGlyArgTrpCysGlyHisLysGlu

586 AGTTCCTCCAAGGATAAAATCAAGAACGAACAAATTAATCAC
 35 ValProProArgIleLysSerArgThrAsnGlnIleLysIleHir

631 ATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT
 PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle
 40 676 TTATTATTCTTTGCTGGAAGATTTCCAACCCGACGAGCTTCAGA
 TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu

721 GACCAACTGGGAATCTGTACAAGCTCTATTCAGGGGTATCCTA
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

5 766 TAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGATGCTCT
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

811 GGACAAAAAATTGCAGAATTGTATACAGTGAAGATCTGCTCAA
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

10 856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

901 TCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAA
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

15 946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

20 991 CAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

1036 GAAGTTGGCCAATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGCA
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

25 1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGTCAACTGGAGGTC
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

1126 CTGCACATGCAATTCAGGGAAAACCGTAAAAAGTATCATGAGGT
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

30 1171 ATTACAGTTTGTAGCCTGGCCACATCAAGAGAGGGGTAGAGCTAA
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys

1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

40 1306 CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTG
1351 AGATAAGAGACCCCTTTCTTACCAGCAACCAAACTTACTACTAGC
1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT

1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTTCTAT
 1486 ACCTAAGAATATAGGATTGCATTTAATAATAGTGTGAGGTTAT
 1531 ATATGCACAAACACACACAGAAATATATTCATGTCATGTGTATA
 1576 TAGATCAAAATGTTTTTTTGGTATATATAACCAGGTACACCAGAG
 5 1621 CTTACATATGTTTGAGTTAGACTCTTAAATCCTTTGCCAAAATA
 1666 AGGGATGGTCAAATATATGAAACATGTCCTTAGAAAATTTAGGAG
 1711 ATAAATTTATTTTAAATTTTGAACACAAAACAATTTGAATCT
 1756 TGCTCTCTTAAAGAAAGCATCTTGTATATTAATAAATCAAAGATG
 1801 AGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:50)

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FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCAT
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA
10 GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTTG
GGGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

15 EVQLVESGGGLVKPGGSLRLSCAASGFNFRITYNMNVWRQAPGKGLEWVSSISS
SSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIIAS
FYFDYWGQGLVTLVSS (SEQ ID NO:13)

C -- Cur2 1.6 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TTTCAGCAGAAACCAGGGAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGATCTGGGACAGA
25 ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:56)

D -- Cur2 1.6 light chain amino acid sequence

30 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWFQKPGKAPKRLIY AASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKEIK (SEQ
ID NO:14)

FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGGTTACCGTCAGTAGCAACTACATGAGC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTTATA
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTC
CAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
10 GAGGACACGGCCGTGTATTACTGTGCGGGAACGGTGACTACGAATTACTACT
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

15 EVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG
GSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAGTVTNNYYGM
DVWGQGTITVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCAAAGTAATGGATAC
AACTATTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAAGTGCCAGT
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
25 TTGGGGTTTATTACTGCATGCAAGCTCTACAACTCTCACTTTCGGCGGAGGG
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

30 DIVMTQSPLSLPVTPGEPASISCRSSQSLQSNNGYNLYLDWYLQKPGQSPQLLIYLG
SNRASGVPRDFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTLTFGGGTKVEI
K (SEQ ID NO:16)

FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

5

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC
TGAGACTCTCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGT
10 ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCAGAGATCAAGGATACAGATATG
CTGGTTACTACTACGACTACGGTATGGACGCTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:59)

15

B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLAEDTAVYYCARDQGYRYA
GYYDYDGMDEVWGQTTTVSS (SEQ ID NO:17)

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C -- Cur2 1.17 light chain nucleotide sequence

25

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAAACAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCGCTCACTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:60)

30

D -- Cur2 1.17 light chain protein sequence

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DIQMTQSPSSLSASVGDRTTTCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
ID NO:18)

FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCAAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
10 ATGACCAAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC
TGGGACATACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:61)

15 B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCASGYFTSYDINWVRQATGQGLEWMGWM
NPNSNGTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIVAG
TYYYYYGMDVWGQTTVTVSS (SEQ D NO:19)

C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
25 TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTCT
GTCTACAGCATAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAAC (SEQ ID NO:62)

30 D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ
35 ID NO:20)

FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGGCACTGGACAAGGCTTGAGTGGATGGGATGGATGAAC
CCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACCA
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
10 ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTTG
GGGGAGTTATCGTGCACTACGGTATGGACGCTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYIFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG
GVIVHYGMDVWGQGTITVTVSS (SEQ ID NO:21)

C -- Cur2 1.19 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAAACAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGCAGTGGATCTGGGACAGA
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTGACCCGTGCAGTTTGGCCAGGGGACCAAGCTGGA
GATCAGAC (SEQ ID NO:64)

D -- Cur2 1.19 light chain amino acid sequence

30 DIQMTQSPSSLSASVGDRTTTCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSDFTLTISLQPEDFATYYCLQHNSDPCSFQGQTKLEIR (SEQ
ID NO:22)

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FIGURE 8

A -- Cur2 1.23 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATACAGATACAGCCCGTCTTCCAAGGCCAGGTCACCA
10 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG
TTTCGGGGAGTTATTATAACGTCCTTTGACTACTGGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

15 EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTR YSPFQGGVITISADKSISTAYLQWSSLKASDTAMY YCARHVSYYVSGS
YYNVFDYWGQGLTVVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGATACAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAACGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
25 GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

DIQMTQSPSSLSASVGVDRVTITCRASQGI RNDLGWYQQIPGKAPKRLIYAASLQR
30 GVPSRFGSGSGTEFTLTITSSLPEDFATYYCLQHNSYPWTFGGQTKVEIK (SEQ
ID NO:24)

FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

5

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCACTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT
ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACC
10 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGGGATACAGCTATG
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:67)

15

B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGYSYG
YVYYDYGMDVWGQGTTVTVSS (SEQ ID NO:25)

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C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
25 TATCAGCAGAAACCAGGGAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAAGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGA
GTTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:68)

30

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQQKPKGAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFLITISLQPEDFATYYCLQHSNYPWTFGQGKTKEIK (SEQ
35 ID NO:26)

FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATACAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG
GTTCGGAGACTTATTATAATGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISKSGSYRFTSYWIGWVRQMPGKGLEWMGIIYPG
DSDTRYSPSQGQVTISADKSISTAYLQWSSLKASDTAMY YCARHGSYYYGSET
YYNVFDYWGQGLTVTVSS (SEQ ID NO:27)

20 C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:70)

30 D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTTTCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:28)

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FIGURE 11

A -- Cur2 1.29 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATACCAGATACAGCCCGTCCCTCCAAGGCCAGGCCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCCCATGTATTACTGTGCGAGACACGTGGATGTAGGGGCT
ACGATTGGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGGCCAAG
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISKKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGG
YYYYYHGMDEVWGQGTITVTVSS (SEQ ID NO:29)

C -- Cur2 1.29 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCC
GGCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCTGATC
25 TATTTGGGTCTAATCGGGCCTCCGGGTCCCTGACAGGTTTCACTGGCAGTGG
ATCAGGCACAGATTTTACTGAAATCAGCAGAGTGGAGGCTGACGATGTT
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTTGGCCA
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

D -- Cur2 1.29 light chain protein sequence

30 DIVMTQSPLSLPVTPEGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLG
SNRASGVPDFRSGSGTDFTLKISRVEADDGVVYCYCMQALQSLMCSFGGQTKL
EIK (SEQ ID NO:30)

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FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

5 CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTTCTCTGCAAGGCTTCTGGTTACACCTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAAACACAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
10 GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCATTACTATGATAGT
AGTGATTATCTCTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCAC
GGTACCCGTCTCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYDSS
DYLYYYYGLDVWVGQGTITVTVSS (SEQ ID NO:31)

20 C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCAC
25 TTGCAATCAGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATT
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAAAGTATAACAGTGCCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGA
TCAAAC (SEQ ID NO:74)

30 D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRTTTCRASQGISNYLAWYQQKPKGVKPLLIYAASLTQ
SGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPLTFGGGTKEIK (SEQ
ID NO:32)

35

FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGCTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGT
ATGATGGAAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT
10 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA
GTGATTATCTCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

15 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWY
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYDSS
DYLYYYYGMDVWGQGTITVTVSS (SEQ ID NO:33)

20 C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAGTCCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACAGGGAAAGTTCCTAACCTCCTGATCTATGCTGCATCCAC
25 TTGCAATCAGGGGTCCCATCTCGGTTCAGTGCCAGTGGATCTGGGACAGATT
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT
CAAAAGTGAACAGTGCCCCGTGGACGTTTCGGCCAAGGGACCACGGTGGAG
ATCAAAAC (SEQ ID NO:76)

30 D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWYQKPKGVPNLLIYAASLTQ
SGVPSRFSGSGSDTFLSLTISSLPEDVAAYYQCQKNSAPWTFGQGTVEIK (SEQ
ID NO:34)

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FIGURE 14

A -- Cur2 1.39.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAACAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATACAGATACAGCCCGTCTTCCAAGGCCAGGTACACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA
ATTCTGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

15 EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIITYPG
DSDTRYSPSFQGGVTTISADKSISTAYLQWSSLKASDTAMYCARHGSIYYNSGS
YYNVFDYWGQGLTVTVSS (SEQ ID NO:35)

20 C -- Cur2 1.39.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCCAGGGAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTTGCAAAAGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:78)

30 D -- Cur2 1.39.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGKTVEIK (SEQ
ID NO:36)

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FIGURE 15

A -- Cur2 1.40.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCACTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCCTAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATGTAGTGGTGGT
AGCTGCTACCAACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDVAVYYCARDIVVVV
AATNYYNGMDVWGQGTITVTVSS (SEQ ID NO:37)

20

FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA
TGTTACGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG
YDYYYGMDVWGQGTITVTVSS (SEQ ID NO:38)

C -- Cur2 1.45 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAATTGCCGGGCGAGTCAGGGCATTAGCAATGATTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCA
25 CTTTGCAATTAGGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGGACAGAT
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG
TCAAAAGTATAACAGTGCCCCATTCACTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:81)

D -- Cur2 1.45 light chain protein sequence

30 DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQ
LGVPSRFSGSGSDFTLTITSLQPEDVATYYCQKYNAPFTFGPGTKVDIK (SEQ
ID NO:39)

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FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAATGGTAACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AACTGCTACGGAATACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSKASGYSFTSYDINWVRQATGQGLEWMGWM
NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARDIVVVVT
ATDYYYGMDVWGQGTITVTVSS (SEQ ID NO:40)

20 C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCAACATCACITGCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACAGGGAAAGCCCCTAAGCGCCTGATTTTGTCTGCATCCA
25 GTTTGCCAAGTGGGGTCCCATCAAGGTTACAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAGTGGTTACCCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:83)

30 D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLWYQKPKGKAPKRLIFAASSLPS
GVPSRFGSGSGTEFTLTISSLQPEDFATYYCLQHSQYPPTFGQGTKEIK (SEQ ID
NO:41)

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FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

5 CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
10 GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGTTGAATATTACTATG
ATGGTAGTGGTTATTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYD
GSGYFFDYWGQGLVTVSS (SEQ ID NO:42)

20 C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGG
TATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA
25 TTTTGCAAAAGTGGGGTCCCATCAAGGTTACAGCGGCAAGTGATCTGGGACAGA
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTGTCATCTTACTATT
GTCAACAGTCTAACAGTTTCCCTCGGACGTTCCGGCCAAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:85)

30 D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRTITCRASQGISSWLAWYQQKPGKAPKLLIYAASILQ
SGVPSRFSGSGSDFTLTIISSLPEDFASYCQQSNSFPRTFGQGTKVEIK (SEQ
ID NO:43)

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FIGURE 19

A -- Cur2 1.49.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTGACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
10 GATCTGAGGACACGGCCGTGATTCTGTGCGAGAATGAGGGATATAGTGGC
TACGAGCTATTACTACTTCTACGGTATGGACGCTCTGGGGCCAAGGGACC
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT
SYYYFYGMDEVWGQGTITVTVSS (SEQ ID NO:44)

20 C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC
25 TATTTGGTTCTAGTCGGGCCTCCGGGTCCCTGACAGGTTCAAGTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAACCTCTACAAACTATCACCTTCGGCCAAGGGA
CACGACTGGAGATTAAC (SEQ ID NO:87)

30 D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPEGEPASISCRSSQSLHSNGYNYLDWYLLKPGQSPQLLIYLG
SSRASGVPDFRSGSGSGTDFTLKISRVEAEDVGVYCYMQTLQITTFGQGTIRLEIK
(SEQ ID NO:45)

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FIGURE 20

A -- Cur2 1.51 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATGCCAAATACAGCCCGTCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTTGA
GGAATTATCGGTATACAGGGTGGTTTCAGCCCTGGGGCCAGGGAACCCTGGT
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDAKYSPSFQGVTVISADKSISTAYLQWSSLKASDTAMYCARHYDVWRNY
RYTGWFDPPWGQGLTVVSS (SEQ ID NO:46)

20 C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCTGTCTTGTCTCCAGGGGAAAG
AGCCACCCTCTCTGCGAGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT
25 CCAACAGGGCCACTGGCATCCCAGACAGGTTACAGTGGCAGTGGGTCTGGGAC
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATT
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTTCGGCCCTGGGACCAAAGT
GATATCAAAC (SEQ ID NO:89)

30 D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA
TGIPDRFSGSGSDFTLTISRLEPEDFAVYYCQQYGSSLTFTFGPGTKVDIK (SEQ
ID NO:47)

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FIGURE 21

A -- Cur2 6.4 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATAAAC
CCTAATAGTGGTAACACAGACTATGCACAGAAGTTCCAGGGCAGAGTCACCA
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGCTTTGGATACAGCTAT
10 AATTACGACTACTATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGGGLEWMGWIN
PNSGNTDYAQKFQGRVTMTDRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY
DYVYGMDVWVGQGITTVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

20 GAAATTGTGTTAGCGAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGTAGTAGTTACTTAGCCT
GGTACCAGCAGAAGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC
CAGCAGGGGCCATGGCATCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACA
GACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTA
CTGTCAGCAGTATGGTAGTTACCGTGCAGTTTTGGCCAGGGGACCAAGCTG
25 GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

30 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAWYQQKPGQAPRLLIYATSSRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPCSFQGQTKLEIK (SEQ
ID NO:49)

FIGURE 22A

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes							
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4	
CR2		V	D	J	V					D & J		
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0	0/0
	VK	mix										
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0

FIGURE 22B

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2											
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V3-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0

FIGURE 24

Figure 24A

										Section 1
										51
Cur2-1.11.1_HC	(1)	1	10	20	30	40				
VH3-53	(1)	EVQLVESGGGLIQPGSSIRLS	SCAASGFTVSSNYMSWVRQAPGKGL	EWVS	VI					
Consensus	(1)	EVQLVESGGGLIQPGSSIRLS	SCAASGFTVSSNYMSWVRQAPGKGL	EWVS	VI					
										Section 2
										102
Cur2-1.11.1_HC	(52)	52	60	70	80	90				
VH3-53	(52)	YSGGSTYYADSVKGRFTISR	DNSENKNTLYLQMN	SLRAEDTAVYYCA	GT	VT	TN			
Consensus	(52)	YSGGSTYYADSVKGRFTISR	DNSENKNTLYLQMN	SLRAEDTAVYYCA	GT	VT	TN			
										Section 3
										120
Cur2-1.11.1_HC	(103)	103	110	120						
VH3-53	(68)	YYGMDVWGQSTTVTS	S							
Consensus	(103)	YYGMDVWGQSTTVTS	S							

Figure 24B

										Section 1
										51
Cur2-1.11.1_LC	(1)	1	10	20	30	40				
A19	(1)	DIVMTQSFLSLPVTGEP	ASISCRSSQSL	LSNGVNYLDWYLQ	KPGQ	SF	QL			
Consensus	(1)	DIVMTQSFLSLPVTGEP	ASISCRSSQSL	LSNGVNYLDWYLQ	KPGQ	SF	QL			
										Section 2
										102
Cur2-1.11.1_LC	(52)	52	60	70	80	90				
A19	(52)	LIYLGSNRRASGVDRF	SGSGSGTDFTLKISR	VEAEDVGVVYCMQAL	Q	LP	--			
Consensus	(52)	LIYLGSNRRASGVDRF	SGSGSGTDFTLKISR	VEAEDVGVVYCMQAL	Q	LP	--			
										Section 3
										111
Cur2-1.11.1_LC	(103)	103	111							
A19	(101)	GGG	TKVEIK							
Consensus	(103)	GGG	TKVEIK							

FIGURE 25

Figure 25A

Section 1									
	(1)	1	10	20	30	40	51		
CR2-1.17.1_HC	(1)	QVQLVESGGGVVQV	QEGKSLRLSCAASGFTFS	SYGMHWVRQAPGKGL	EWVA	VI			
VH3-33	(1)	QVQLVESGGGVVQV	QEGKSLRLSCAASGFTFS	SYGMHWVRQAPGKGL	EWVA	VI			
Consensus	(1)	QVQLVESGGGVVQV	QEGKSLRLSCAASGFTFS	SYGMHWVRQAPGKGL	EWVA	VI			
Section 2									
	(52)	52	60	70	80	90	102		
CR2-1.17.1_HC	(52)	WYDGSNKYYADSVK	GRFTISRDN	SKNTLYIQMNSL	RAEDTA	VVYCAR	QGY		
VH3-33	(52)	WYDGSNKYYADSVK	GRFTISRDN	SKNTLYIQMNSL	RAEDTA	VVYCAR	---		
Consensus	(52)	WYDGSNKYYADSVK	GRFTISRDN	SKNTLYIQMNSL	RAEDTA	VVYCAR			
Section 3									
	(103)	103	110	126					
CR2-1.17.1_HC	(103)	RYAGYYDYGMDV	NGQTTVT	VSS					
VH3-33	(99)	-----							
Consensus	(103)								

Figure 25B

Section 1									
	(1)	1	10	20	30	40	52		
CR2-1.17.1_LC	(1)	DIQMTQSPPSLSASV	GDVRVITCRASQGI	RNDLGMWYQQK	FGKAPKRLI	YAA	S		
A30	(1)	DIQMTQSPPSLSASV	GDVRVITCRASQGI	RNDLGMWYQQK	FGKAPKRLI	YAA	S		
Consensus	(1)	DIQMTQSPPSLSASV	GDVRVITCRASQGI	RNDLGMWYQQK	FGKAPKRLI	YAA	S		
Section 2									
	(53)	53	60	70	80	90	104		
CR2-1.17.1_LC	(53)	SIQSGVPSRFSGSG	SGTEFTLTIS	SLQPEDFATYYC	LQHN	SYPLT	FGGGTRV		
A30	(53)	SIQSGVPSRFSGSG	SGTEFTLTIS	SLQPEDFATYYC	LQHN	SYPLT	FGGGTRV		
Consensus	(53)	SIQSGVPSRFSGSG	SGTEFTLTIS	SLQPEDFATYYC	LQHN	SYPLT	FGGGTRV		
Section 3									
	(105)	105	107						
CR2-1.17.1_LC	(105)	EIK							
A30	(96)	---							
Consensus	(105)								

FIGURE 26

Figure 26A

Section 1									
	(1)	1	10	20	30	40	50	60	70
CR2-1.18_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINMVRQATGGGLEMMGMN							
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINMVRQATGGGLEMMGMN							
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINMVRQATGGGLEMMGMN							
Section 2									
	(53)	53	60	70	80	90	100	110	120
CR2-1.18_HC	(53)	FNHSGNTGYAQRFGQRTVMTNRTSISTAYMELSSLSRSEDYAVYYCAREGIAVA							
VH1-8	(53)	FNHSGNTGYAQRFGQRTVMTNRTSISTAYMELSSLSRSEDYAVYYCAR-----							
Consensus	(53)	FNHSGNTGYAQRFGQRTVMTNRTSISTAYMELSSLSRSEDYAVYYCAR							
Section 3									
	(105)	105	110	120	130	140	150	160	170
CR2-1.18_HC	(105)	GTYYYYYNDVHGQGTTVTVSS							
VH1-8	(99)	-----							
Consensus	(105)	GTYYYYYNDVHGQGTTVTVSS							

Figure 26B

Section 1									
	(1)	1	10	20	30	40	50	60	70
CR2-1.18_LC	(1)	DIQMTQSPFSSLSASVGDRTVITCRASQGIIRNDLGHYQKRPGRAPKRLIYAASS							
A30	(1)	DIQMTQSPFSSLSASVGDRTVITCRASQGIIRNDLGHYQKRPGRAPKRLIYAASS							
Consensus	(1)	DIQMTQSPFSSLSASVGDRTVITCRASQGIIRNDLGHYQKRPGRAPKRLIYAASS							
Section 2									
	(54)	54	60	70	80	90	100	110	120
CR2-1.18_LC	(54)	IQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSTPFTFGPGTKVDI							
A30	(54)	IQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSTPFTFGPGTKVDI							
Consensus	(54)	IQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSTP							
Section 3									
	(107)	107	110	120	130	140	150	160	170
CR2-1.18_LC	(107)	K							
A30	(96)	-							
Consensus	(107)	K							

FIGURE 27

Figure 27A

Section 1					
(1)	1	10	20	30	40
Cur2-1.19.1_hc	(1)	QVQLVQSGAEVVKFPGASVKV	CKASGYTFTSYDINHW	ROATGQGLENNMGNH	52
VH1-8	(1)	QVQLVQSGAEVVKFPGASVKV	CKASGYTFTSYDINHW	ROATGQGLENNMGNH	
Consensus	(1)	QVQLVQSGAEVVKFPGASVKV	CKASGYTFTSYDINHW	ROATGQGLENNMGNH	
Section 2					
(53)	53	60	70	80	90
Cur2-1.19.1_hc	(53)	PNSGNTGYAQRFGSRVTMT	RNTSISTAYMELSSLR	SEDAVYYCARDVMITF	104
VH1-8	(53)	PNSGNTGYAQRFGSRVTMT	RNTSISTAYMELSSLR	SEDAVYYCAR-----	
Consensus	(53)	PNSGNTGYAQRFGSRVTMT	RNTSISTAYMELSSLR	SEDAVYYCAR	
Section 3					
(105)	105	110	126		
Cur2-1.19.1_hc	(105)	GGVIVHYGMDVWGQGT	TTVTS		
VH1-8	(99)	-----			
Consensus	(105)				

Figure 27B

Section 1					
(1)	1	10	20	30	40
Cur2-1.19.1_ic	(1)	DIQMTQSPFSSLSASVGD	RVITTCRA	SCGIRNDL	GWYQQKPKAPKRLIYAAS
A30	(1)	DIQMTQSPFSSLSASVGD	RVITTCRA	SCGIRNDL	GWYQQKPKAPKRLIYAAS
Consensus	(1)	DIQMTQSPFSSLSASVGD	RVITTCRA	SCGIRNDL	GWYQQKPKAPKRLIYAAS
Section 2					
(53)	53	60	70	80	90
Cur2-1.19.1_ic	(53)	SLQSGVPSRFSGSGSGTD	FTLTISSLQPEDFAT	YVCLQHN	SDPCFSGQGT
A30	(53)	SLQSGVPSRFSGSGSGTD	FTLTISSLQPEDFAT	YVCLQHN	SDPCFSGQGT
Consensus	(53)	SLQSGVPSRFSGSGSGTD	FTLTISSLQPEDFAT	YVCLQHN	SDPCFSGQGT
Section 3					
(105)	105	106	107		
Cur2-1.19.1_ic	(105)	EIR			
A30	(96)	---			
Consensus	(105)				

FIGURE 28

Figure 28A

Section 1							
	(1)	1	10	20	30	40	51
Cur2-1.23.1_HC	(1)	EVQLVQSGAEVKKPGEGLKISCSGSGYFTSTYWGIVRMPFGKGLEWNGII					
VH5-51	(1)	EVQLVQSGAEVKKPGEGLKISCSGSGYFTSTYWGIVRMPFGKGLEWNGII					
Consensus	(1)	EVQLVQSGAEVKKPGEGLKISCSGSGYFTSTYWGIVRMPFGKGLEWNGII					
Section 2							
	(52)	52	60	70	80	90	102
Cur2-1.23.1_HC	(52)	YFGDSDFTRYSPFQGVTTISADKSIISTAYLQWSSSLKASDTAMYVCARHVS					
VH5-51	(52)	YFGDSDFTRYSPFQGVTTISADKSIISTAYLQWSSSLKASDTAMYVCAR----					
Consensus	(52)	YFGDSDFTRYSPFQGVTTISADKSIISTAYLQWSSSLKASDTAMYVCAR					
Section 3							
	(103)	103	110	126			
Cur2-1.23.1_HC	(103)	YYVSGSYNVFDYWGQGTITVTVSS					
VH5-51	(99)	-----					
Consensus	(103)						

Figure 28B

Section 1							
	(1)	1	10	20	30	40	51
Cur2-1.23.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDIGWYQQIFPKAKRLIYAA					
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDIGWYQQIFPKAKRLIYAA					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDIGWYQQIFPKAKRLIYAA					
Section 2							
	(52)	52	60	70	80	90	102
Cur2-1.23.1_LC	(52)	SSLQGVSPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNISYPMTFGQET					
A30	(52)	SSLQGVSPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNISYP-----					
Consensus	(52)	SSLQGVSPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNISYP					
Section 3							
	(103)	103	107				
Cur2-1.23.1_LC	(103)	KVEIK					
A30	(96)	----					
Consensus	(103)						

FIGURE 29

Figure 29A

							Section 1
	(1)	1	10	20	30	40	51
CR2-1.24.1_HC	(1)	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVA					I
VH3-33	(1)	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVA					I
Consensus	(1)	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVA					I
							Section 2
	(52)	52	60	70	80	90	102
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					DQSY
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					---
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					---
							Section 3
	(103)	103	110	126			
CR2-1.24.1_HC	(103)	SYGVVYDYGMDVWGQGT					TVTS
VH3-33	(99)	-----					---
Consensus	(103)	SYGVVYDYGMDVWGQGT					TVTS

Figure 29B

							Section 1
	(1)	1	10	20	30	40	52
CR2-1.24.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI					RNDLGWYQQKPKGAPKRLIYAAS
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI					RNDLGWYQQKPKGAPKRLIYAAS
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI					RNDLGWYQQKPKGAPKRLIYAAS
							Section 2
	(53)	53	60	70	80	90	104
CR2-1.24.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHN					SYWTFGGQTKV
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHN					SYWTFGGQTKV
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHN					SYWTFGGQTKV
							Section 3
	(105)	1067					
CR2-1.24.1_LC	(105)	EIK					
A30	(95)	---					
Consensus	(105)	EIK					

FIGURE 30

Figure 30A

Section 1						
	(1)	10	20	30	40	51
VH5-51	(1)	EVQLVQSGAEVKKPQGSFLKISCKKSGSYFTSYWIGMVRQMPKGLNWMGII				
CR2-1.25.1_HC	(1)	EVQLVQSGAEVKKPQGSFLKISCKKSGSYFTSYWIGMVRQMPKGLNWMGII				
Consensus	(1)	EVQLVQSGAEVKKPQGSFLKISCKKSGY FTSYWIGMVRQMPKGLNWMGII				
Section 2						
	(52)	52	60	70	80	90
VH5-51	(52)	YFGSDSDTRYSPSFQSGVTTISADKSIISTAYLQWSSSLKASDTANYTCAR---				
CR2-1.25.1_HC	(52)	YFGSDSDTRYSPSFQSGVTTISADKSIISTAYLQWSSSLKASDTANYTCARHGSY				
Consensus	(52)	YFGSDSDTRYSPSFQSGVTTISADKSIISTAYLQWSSSLKASDTANYTCAR				
Section 3						
	(103)	103	110	126		
VH5-51	(99)	-----				
CR2-1.25.1_HC	(103)	YYGSSTYYNVVDYWGQSTLVTVSS				
Consensus	(103)					

Figure 30B

Section 1							
	(1)	1	10	20	30	40	52
A30	(1)	DIQMTQSPSSLSASVGDRAVITTCRASQGIIRNDLGMVYQQRFGKAPRLIYAAS					
CR2-1.25.1_LC	(1)	DIQMTQSPSSLSASVGDRAVITTCRASQGIIRNDLGMVYQQRFGKAPRLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRAVITTCRASQGIIRNDLGMVYQQRFGKAPRLIYAAS					
Section 2							
	(53)	53	60	70	80	90	104
A30	(53)	SIQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCIQHNSYP-----					
CR2-1.25.1_LC	(53)	SIQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCIQHNSYPWTFGQGTWK					
Consensus	(53)	SIQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCIQHNSYP					
Section 3							
	(105)	1097					
A30	(96)	---					
CR2-1.25.1_LC	(105)	EIK					
Consensus	(105)						

FIGURE 31

Figure 31A

Section 1					
	(1)	10	20	30	40 52
VH5-51	(1)	EVQLVQSGAEVKKP	GESLKI	SCRGSGYSFT	SYWIGVVRQMPGK
CR2-1.29_HC	(1)	EVQLVQSGAEVKKP	GESLKI	SCRGSGYSFT	SYWIGVVRQMPGK
Consensus	(1)	EVQLVQSGAEVKKP	GESLKI	SCRGSGYSFT	SYWIGVVRQMPGK
Section 2					
	(53)	60	70	80	90 104
VH5-51	(53)	PGDS	SDTRYSP	FQGGV	TISADK
CR2-1.29_HC	(53)	PGDS	SDTRYSP	FQGGV	TISADK
Consensus	(53)	PGDS	SDTRYSP	FQGGV	TISADK
Section 3					
	(105)	105	110	129	
VH5-51	(98)	-----	-----	-----	
CR2-1.29_HC	(105)	TIGG	YVYVYH	GMDV	WGQGT
Consensus	(105)	TIGG	YVYVYH	GMDV	WGQGT

Figure 31B

Section 1					
	(1)	10	20	30	40 53
A19	(1)	DI	VMTQ	SFLS	LPVTP
CR2-1.29_LC	(1)	DI	VMTQ	SFLS	LPVTP
Consensus	(1)	DI	VMTQ	SFLS	LPVTP
Section 2					
	(54)	54	60	70	80 90 105
A19	(54)	YLG	SNR	ASGV	PD
CR2-1.29_LC	(54)	YLG	SNR	ASGV	PD
Consensus	(54)	YLG	SNR	ASGV	PD
Section 3					
	(107)	107	113		
A19	(101)	-----	-----		
CR2-1.29_LC	(107)	ST	KLEIK		
Consensus	(107)	ST	KLEIK		

FIGURE 32

Figure 32A

Section 1					
	(1)	10	20	30	40
VH1-18	(1)	QVQLVQSGAEVKKPQASVKVSCKASGVTFTTSYGIINVRQAPGGGLENNMGWIS			52
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPQASVKVSCKASGVTFTTSYGIINVRQAPGGGLENNMGWIS			
Consensus	(1)	QVQLVQSGAEVKKPQASVKVSCKASGVTFTTSYGIINVRQAPGGGLENNMGWIS			
Section 2					
	(53)	60	70	80	90
VH1-18	(53)	AYNGHTNYAQRLOGRAVTMTDTSTSTAYMELRSLRSDDTAVVYCAR-----			104
CR2-1.33_HC	(53)	AYNGHTNYAQRLOGRAVTMTDTSTSTAYMELRSLRSDDTAVVYCARDHYDSS			
Consensus	(53)	AYNGHTNYAQRLOGRAVTMTDTSTSTAYMELRSLRSDDTAVVYCAR			
Section 3					
	(105)	105	110	127	
VH1-18	(99)	SDYLYYYYGLDVMGGQTFTVTS			
CR2-1.33_HC	(105)	SDYLYYYYGLDVMGGQTFTVTS			
Consensus	(105)				

Figure 32B

Section 1					
	(1)	10	20	30	40
A20	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS			53
CR2-1.33_LC	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS			
Consensus	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS			
Section 2					
	(54)	54	60	70	80
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISISLOPEDVATVYCCQYNAP-----			106
CR2-1.33_LC	(54)	LQSGVPSRFSGSGSGTDFTLTISISLOPEDVATVYCCQYNAPLTFGGGKTVKI			
Consensus	(54)	LQSGVPSRFSGSGSGTDFTLTISISLOPEDVATVYCCQYNAP			
Section 3					
	(107)	107			
A20	(96)	-			
CR2-1.33_LC	(107)	K			
Consensus	(107)				

FIGURE 33

Figure 33A

Section 1					
	(1)	10	20	30	40
VH3-33	(1)	QVQLVESGGGVVQEGASRLSCAASGPTFSYGMHWVRQAPGKLEWVAII			51
CR2-1.38.1_HC	(1)	QVQLVESGGGVVQEGASRLSCAASGPTFSYGMHWVRQAPGKLEWVAII			
Consensus	(1)	QVQLVESGGGVVQEGASRLSCAASGPTFSYGMHWVRQAPGKLEWVAII			
Section 2					
	(52)	60	70	80	90
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRADTAIVYCAR----			102
CR2-1.38.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRADTAIVYCAR----			
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNSEKNTLYLQMNSLRADTAIVYCAR			
Section 3					
	(103)	110	127		
VH3-33	(99)	-----			
CR2-1.38.1_HC	(103)	DSSDYLYYYGMDVWGQGTITVTS			
Consensus	(103)				

Figure 33B

Section 1					
	(1)	10	20	30	40
A20	(1)	DIQMTQSPFSLASVSGDRVTITCRASQGISNFWLAWYQQKPKGKVPKLLIYAA			52
CR2-1.38.1_LC	(1)	DIQMTQSPFSLASVSGDRVTITCRASQGISNFWLAWYQQKPKGKVPKLLIYAA			
Consensus	(1)	DIQMTQSPFSLASVSGDRVTITCRASQGISNFWLAWYQQKPKGKVPKLLIYAA			
Section 2					
	(53)	60	70	80	90
A20	(53)	TLCSGVPSRFSGSSTDTFELTISGLQPEDVAAYYCKVNSAP-----			104
CR2-1.38.1_LC	(53)	TLCSGVPSRFSGSSTDTFELTISGLQPEDVAAYYCKVNSAP-----			
Consensus	(53)	TLCSGVPSRFSGSSTDTFELTISGLQPEDVAAYYCKVNSAP			
Section 3					
	(105)	1067			
A20	(96)	---			
CR2-1.38.1_LC	(105)	EIK			
Consensus	(105)				

FIGURE 34

Figure 34A

	(1)	10	20	30	40	51
VH5-51	(1)	EVQLVQSGAEVKKPQGS	SLKISCKGSGYSPTSYWIGWVRQMPGKGLEMMGII			
CR2-139.1_HC	(1)	EVQLVQSGTEVKKPQGS	SLKISCKGSGYRFTSYWIGWVRQMPGKGLEMMGII			
Consensus	(1)	EVQLVQSG	EVKKPQGS	SLKISCKGSGY	FTSYWIGWVRQMPGKGLEMMGII	
	(52)	60	70	80	90	102
VH5-51	(52)	YFGDSDDTRYSPFQSGQVTISADKSI	STAYLQWSSLKASDTAMYYCAR---			
CR2-139.1_HC	(52)	YFGDSDDTRYSPFQSGQVTISADKSI	STAYLQWSSLKASDTAMYYCARHGSY			
Consensus	(52)	YFGDSDDTRYSPFQSGQVTISADKSI	STAYLQWSSLKASDTAMYYCAR			
	(103)	110	126			
VH5-51	(99)	-----	-----			
CR2-139.1_HC	(103)	YYNSGSYYNVFDYMGQSTLVTS				
Consensus	(103)					

Figure 34B

	(1)	10	20	30	40	52
A30	(1)	DIQMTQSPFSSLSASVGDRAVITCRASQ	SRINDLGWYQKPKAPRLIIYAAS			
CR2-139.1_LC	(1)	DIQMTQSPFSSLSASVGDRAVITCRASQ	SRINDLGWYQKPKAPRLIIYAAS			
Consensus	(1)	DIQMTQSPFSSLSASVGDRAVITCRASQ	SRINDLGWYQKPKAPRLIIYAAS			
	(53)	60	70	80	90	104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISIQ	EDFATYYCLOHNSYP-----			
CR2-139.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISIQ	EDFATYYCLOHNSYVMTFGQGTKV			
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISIQ	EDFATYYCLOHNSYP			
	(105)	1997				
A30	(96)	---				
CR2-139.1_LC	(105)	BIK				
Consensus	(105)					

FIGURE 35

Figure 35A

	(1)	10	20	30	40	52	Section 1
VH1-8	(1)	QVQLVQSGAEVKRFGASVKVSCKASGYTF	TSYDINHWVROATGGGLEWMGWMN				
CR2-145_HC	(1)	QVQLVQSGAEVKRFGASVKVSCKASGYTF	TSYDINHWVROATGGGLEWMGWMN				
Consensus	(1)	QVQLVQSGAEVKRFGASVKVSCKASGYTF	TSYDINHWVROATGGGLEWMGWMN				
	(53)	60	70	80	90	104	Section 2
VH1-8	(53)	PNSGNTGYAQRFGGRVMTNRT	SISTAYMELSSLRSEDTAVYYCAR	-----			
CR2-145_HC	(53)	PNSGNTGYAQRFGGRVMTNRT	SISTAYMELSSLRSEDTAVYYCAR	GGGY	SY		
Consensus	(53)	PNSGNTGYAQRFGGRVMTNRT	SISTAYMELSSLRSEDTAVYYCAR				
	(105)	105	110	125			Section 3
VH1-8	(99)	-----					
CR2-145_HC	(105)	GYDYYYGMDVWGQGT	TVTVSS				
Consensus	(105)						

Figure 35B

	(1)	10	20	30	40	53	Section 1
A20	(1)	DIQMTQSPSSLSASVGRVTITCRASQGIS	SNLANYQQRPGKVPKLLIYAAS				
CR2-145_LC	(1)	DIQMTQSPSSLSASVGRVTINCRASQGIS	SNLANYQQRPGKVPKLLIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGRVTI	CRASQGISN	LANYQQRPGKVPKLLIYAAS			
	(54)	60	70	80	90	106	Section 2
A20	(54)	LQSGVSRFSGSGSGTDFTLTIS	SLQPEDVATYYCQYN	SAP	-----		
CR2-145_LC	(54)	LQLGVSRFSGSGSGTDFTLTIS	SLQPEDVATYYCQYN	SAP	TPGPGTKVDI		
Consensus	(54)	LQ	GVS	SRFSGSGSGTDFTLTIS	SLQPEDVATYYCQYN	SAP	
	(107)	107					Section 3
A20	(96)	-					
CR2-145_LC	(107)	K					
Consensus	(107)						

5

10

FIGURE 36

Figure 36A

	(1)	10	20	30	40	51
VH1-8	(1)	QVQLVQSGAEVKKFGASVKVSCKASGYTF	TSYDINMWVRQATCGGLENNMGWM			
CR2-1.46.1_HC	(1)	QVQLVQSGAEVKKFGASVKVSCKASGYTF	TSYDINMWVRQATCGGLENNMGWM			
Consensus	(1)	QVQLVQSGAEVKKFGASVKVSCKASGYTF	TSYDINMWVRQATCGGLENNMGWM			
	(52)	60	70	80	90	102
VH1-8	(52)	NPNSGNTGYAQKFQGRVTMTNTSISTAYNELSSLRSEDTAVYYCAR---				
CR2-1.46.1_HC	(52)	NPNSGNTGYAQKFQGRVTMTNTSISTAYNELSSLRSEDTAVYYCARDIVV				
Consensus	(52)	NPNSGNTGYAQKFQGRVTMTNTSISTAYNELSSLRSEDTAVYYCAR				
	(103)	110	126			
VH1-8	(99)	-----				
CR2-1.46.1_HC	(103)	VVTAIDYYYGMDVHGQSTTVTVSS				
Consensus	(103)					

Figure 36B

	(1)	10	20	30	40	52
A30	(1)	DIQMTQSPFSLASVGDRTITCRASQGI	NDLGWYQQKPKAPRLIYAAS			
CR2-1.46.1_LC	(1)	DIQMTQSPFSLASVGDRTITCRASQGI	NDLGWYQQKPKAPRLIYAAS			
Consensus	(1)	DIQMTQSPFSLASVGDRTITCRASQGI	NDLGWYQQKPKAPRLIYAAS			
	(53)	60	70	80	90	104
A30	(53)	SLQSGVSRFSGSGSTFTLTISIQPEDFATYYC	LQHNRYF-----			
CR2-1.46.1_LC	(53)	SLQSGVSRFSGSGSTFTLTISIQPEDFATYYC	LQHNRYF-----			
Consensus	(53)	SLQSGVSRFSGSGSTFTLTISIQPEDFATYYC	LQHNRYF-----			
	(105)	1067				
A30	(98)	---				
CR2-1.46.1_LC	(105)	ETK				
Consensus	(105)					

Figure 38A

	(1)	10	20	30	40	51	Section 1
CR2-149.1_HC	(1)	QVQLVQSGAEVKKPGASVVKSCASGYTFTSYDINHWNRQATQGQLEWNGMGR					
VH1-6	(1)	QVQLVQSGAEVKKPGASVVKSCASGYTFTSYDINHWNRQATQGQLEWNGMGR					
Consensus	(1)	QVQLVQSGAEVKKPGASVVKSCASGYTFTSYDINHWNRQATQGQLEWNGMGR					
	(52)	52	60	70	80	90	102
CR2-149.1_HC	(52)	NPNNGDTGYAQKFGQRVMTTRNTISITAYMELSSLRSEDVAVYFCARMDR					
VH1-8	(52)	NPNNGDTGYAQKFGQRVMTTRNTISITAYMELSSLRSEDVAVYFCARMDR					
Consensus	(52)	NPNNGDTGYAQKFGQRVMTTRNTISITAYMELSSLRSEDVAVYFCAR					
	(103)	103	110	127			Section 3
CR2-149.1_HC	(103)	VATSYYYYPVGMVGVGVTVTVTVSS					
VH1-8	(99)	-----					
Consensus	(103)	-----					

Figure 38B

	(1)	10	20	30	40	52	Section 1
CR2-149_1.LC	(1)	DIUMTQSP	LSLPVTP	GEPASIS	ICRSRGS	QLSHNGNY	DWYLDYLK
A19	(1)	DIVMTQSP	LSLPVTP	GEPASIS	ICRSRGS	QLSHNGNY	DWYLDYLK
Consensus	(1)	DIVMTQSP	LSLPVTP	GEPASIS	ICRSRGS	QLSHNGNY	DWYLDYLK
	(53)	YLG	SSRAS	GVDP	RGSG	SGSDFT	LKISR
CR2-149_1.LC	(53)	YLG	SSRAS	GVDP	RGSG	SGSDFT	LKISR
A19	(53)	YTLG	SNRAS	GVDP	RGSG	SGSDFT	LKISR
Consensus	(53)	YTLG	SNRAS	GVDP	RGSG	SGSDFT	LKISR
	(105)	105	111				
CR2-149_1.LC	(105)	GRLEIK					
A19	(101)	GRLEIK					
Consensus	(105)	GRLEIK					

FIGURE 39

Figure 39A

	(1)	10	20	30	40	51
CR2-151.1_HC	(1)	EVQLVQSGAEVKKPESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
VH5-51	(1)	EVQLVQSGAEVKKPESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKPESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
	(52)	60	70	80	90	102
CR2-151.1_HC	(52)	YFGSDDAKYSPPSFQGGVTISADKKSISTAYLQWSSSLKASDTAMYYCARHYDY				
VH5-51	(52)	YFGSDSDTRYSPSFQGGVTISADKKSISTAYLQWSSSLKASDTAMYYCAR----				
Consensus	(52)	YFGSDSD KYSPPSFQGGVTISADKKSISTAYLQWSSSLKASDTAMYYCAR				
	(103)	110	126			
CR2-151.1_HC	(103)	VWRNRYRTGMFDFWGQSTLVTVS				
VH5-51	(99)	-----				
Consensus	(103)					

Figure 39B

	(1)	10	20	30	40	52
CR2-151.1_LC	(1)	EIVLTQSPGTLISLSPGERATLSCRAQSQVSSSYLAWYQQRPGQAPRLIIYA				
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRAQSQVSSSYLAWYQQRPGQAPRLIIYA				
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRAQSQVSSSYLAWYQQRPGQAPRLIIYA				
	(53)	60	70	80	90	104
CR2-151.1_LC	(53)	SNRATGIPDRFSGSGSTDPFTLTISRLPEDFAVYYCQYQSSSLPTFGSEK				
A27	(53)	SNRATGIPDRFSGSGSTDPFTLTISRLPEDFAVYYCQYQSSSLPTFGSEK				
Consensus	(53)	SNRATGIPDRFSGSGSTDPFTLTISRLPEDFAVYYCQYQSSSLPTFGSEK				
	(105)	108	08			
CR2-151.1_LC	(105)	VDIK				
A27	(97)	----				
Consensus	(105)					

FIGURE 40

Figure 40A

	Section 1									
	(1)	10	20	30	40	50				
Cu2-6.4.1_hc	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF	TSYDINNWVRQATGQGLEWMHGM	TN						
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF	TSYDINNWVRQATGQGLEWMHGM	TN						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF	TSYDINNWVRQATGQGLEWMHGM	TN						
	Section 2									
	(53)	53	60	70	80	90	100	104		
Cu2-6.4.1_hc	(53)	PNSGNTDYAQKFGSRVTMRDTSISTAYNELSSLRS	EDTAIYYCVRGFGYSY							
VH1-8	(53)	PNSGNTGYAQRFGSRVTMRNTSISTAYNELSSLRS	EDTAIYYCAR	-----						
Consensus	(53)	PNSGNT YAQKFGSRVTMR T	SI	STAYNELSSLRS	EDTAIYYG	R				
	Section 3									
	(105)	105	110	125						
Cu2-6.4.1_hc	(105)	NYDYVYVGM	DMVWGQGT	TVTVSS						
VH1-8	(99)	-----								
Consensus	(105)									

Figure 40B

							Section 1
	(1)	10	20	30	40	50	
Cu2-6.4.1 Lc	(1)	EIVLTQSPG	TLSLSPGERATL	SCRASQSV	SSSYLA	WYQKPGQAPRL	LIVAT
A27	(1)	EIVLTQSPG	TLSLSPGERATL	SCRASQSV	SSSYLA	WYQKPGQAPRL	LIVAT
Consensus	(1)	EIVLTQSPG	TLSLSPGERATL	SCRASQSV	SSSYLA	WYQKPGQAPRL	LIVAT
							Section 2
	(53)	53	60	70	80	90	104
Cu2-6.4.1 Lc	(53)	SSRATGIPDR	FSGSGSGTD	FTLTISRL	EPEDFAVY	CCQYGS	SPCSFG
A27	(53)	SSRATGIPDR	FSGSGSGTD	FTLTISRL	EPEDFAVY	CCQYGS	SPCSFG
Consensus	(53)	SSRATGIPDR	FSGSGSGTD	FTLTISRL	EPEDFAVY	CCQYGS	SP
							Section 3
	(105)	105	108				
Cu2-6.4.1 Lc	(105)	LEIK					
A27	(97)	---					
Consensus	(105)						

FIGURE 41

CLONE #	VH	#DE L	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH # del	JH Segment
1.19.1	DP-15/1-8	-1	CGAGG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B -12	ACTACG (SEQ ID NO:94)
1.19.2	DP-15/1-8	-1	CGAGG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B -12	ACTACG (SEQ ID NO:94)
1.19.3	DP-15/1-8	-1	CGAGG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B -12	ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B 0	ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B 0	ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B 0	ATTACTAC (SEQ ID NO:97)

CLONE	vk	#de I	vk end	#n	N SEQ	Jk	# del	Jk end
1.19.1	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.2	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.3	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
6.4.1	A27/A27A	-3	CTCACC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)

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6.4.2	A27/A27A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)

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FIGURE 42

CLONE #	VH	#DEL	VH END (SEQ ID NO:104)	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.6.1	DP-77/3-21	0	GAGACA (SEQ ID NO:104)	0	0	D3-16	22	TATATGATTAC GTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGGT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGACA (SEQ ID NO:104)	0	0	D3-16	22	TATATGATTAC GTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGGT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGACA (SEQ ID NO:104)	0	0	D3-16	22	TATATGATTAC GTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGGT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGACA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.11.2	DP-42/3-53	-5	AGACA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)

CLONE	Vk	#del	Vk end	#n	N SEQ	Jk	# del	Jk end
1.6.1	A30	-3	TTACCC (SEQ ID NO:104)	0	0	JK4	0	GCTCACT (SEQ ID NO:105)

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1.6.2	A30	-3	TTACCC (SEQ ID NO:116)	0		JK4	0	NO:117) GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TTCACTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TTCACTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)

FIGURE 43

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D6-19	19	GGGTATAG CAGTGGCT GG (SEQ ID NO:126)	4	GACA (SEQ ID NO:123)	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT (SEQ ID NO:130)	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT (SEQ ID NO:130)	JH6B	-4	CTACTA (SEQ ID NO:130)
1.25.1	DP-75/5-51	0	GAGAGA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GATATATTA TGGTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT (SEQ ID NO:134)	JH4B	-4	CTTTGA (SEQ ID NO:135)

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CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATTATTA TGGTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:134)
1.29	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTGGATGT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT (SEQ ID NO:137)	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTC (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATAATTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.39.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATAATTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.40.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:147)	0	0	D2	25	ATATTGTA GTGGTGGT	2	CA	JH6B	-6	ACTACT (SEQ ID NO:151)

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CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
			NO:151)					AGCTGCTA C (SEQ ID NO:152)					NO:153)
1.40.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-15/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)

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CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG A TGGCTACG (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG A TGGCTACG (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGa GGaATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGa GGaATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
-------	----	------	--------	----	-------	----	-------	--------

1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)

2023-03-03

CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
1.18	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK3	0	ATTACAC (SEQ ID NO:173)
1.24.1	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK1	0	GTGGAC (SEQ ID NO:175)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.25.1	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:180)	0	0	JK1	0	GTGGAC (SEQ ID NO:181)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:182)	14	TTCTCTCATG TGCAG (SEQ ID NO:183)	JK2	-7	TTTTGG (SEQ ID NO:184)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK4	0	GCTCAC (SEQ ID NO:186)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.39.1	A30	3	TTACCC (SEQ ID NO:189)	0	0	JK1	0	GTGGAC (SEQ ID NO:190)
1.39.2	A30	3	TTACCC (SEQ ID NO:191)	0	0	JK1	0	GTGGAC (SEQ ID NO:192)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:193)	0	0	JK3	0	ATTACAC (SEQ ID NO:194)
1.46.1	A30	0	CCCTCC (SEQ ID NO:195)	0	0	JK1	-3	GACGTT (SEQ ID NO:196)

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CLONE	vk	#del	vk end	#n	N SEQ	JK	# del	JK end
			NO:1911)					NO:1921)
1.46.2	A30	0	CCCTGC (SEQ ID NO:1911)	0	0	JK1	-3	GACGTT (SEQ ID NO:1921)
1.48.1	L5/DPK5V	1	TCCCTC (SEQ ID NO:1931)	0	0	JK1	-2	GGAGGTT (SEQ ID NO:1941)
1.48.2	L5/DPK5V	1	TCCCTC (SEQ ID NO:1931)	0	0	JK1	-2	GGAGGTT (SEQ ID NO:1941)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:1951)	0	0	JK5	-1	ATCAAC (SEQ ID NO:1961)
1.49.2	A3/A19/DPK	5	CAAACT (SEQ ID NO:1951)	0	0	JK5	-1	ATCAAC (SEQ ID NO:1961)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:1971)	1	T	JK3	0	ATTAC (SEQ ID NO:1981)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:1971)	1	T	JK3	0	ATTAC (SEQ ID NO:1981)

FIGURE 44

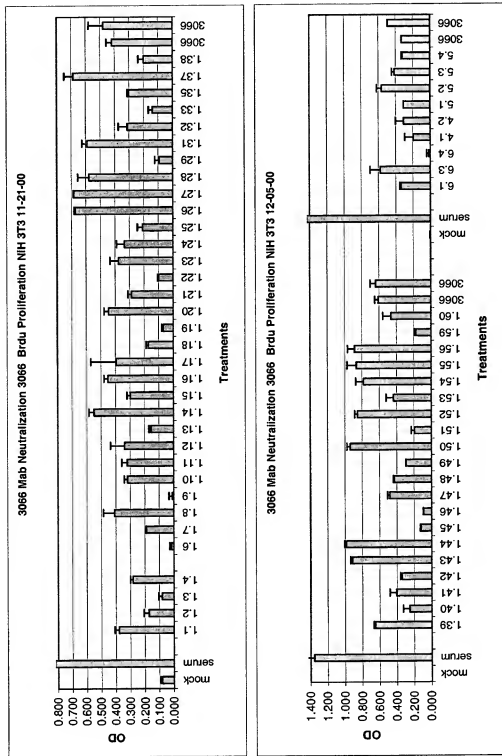


FIGURE 45

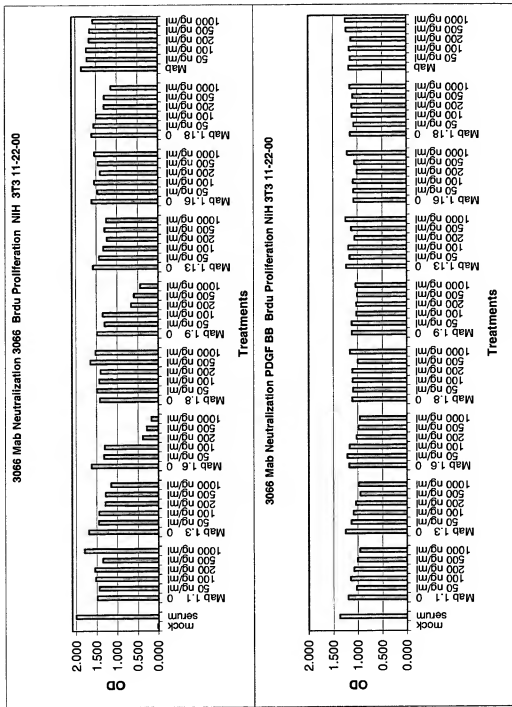


FIGURE 46

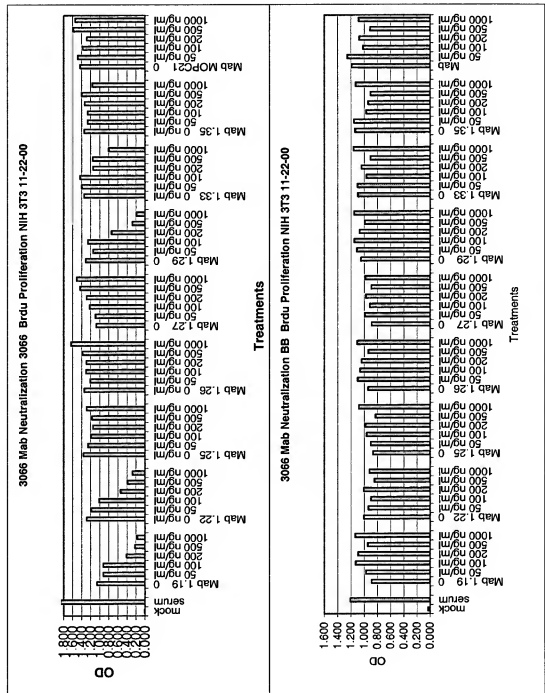


FIGURE 47

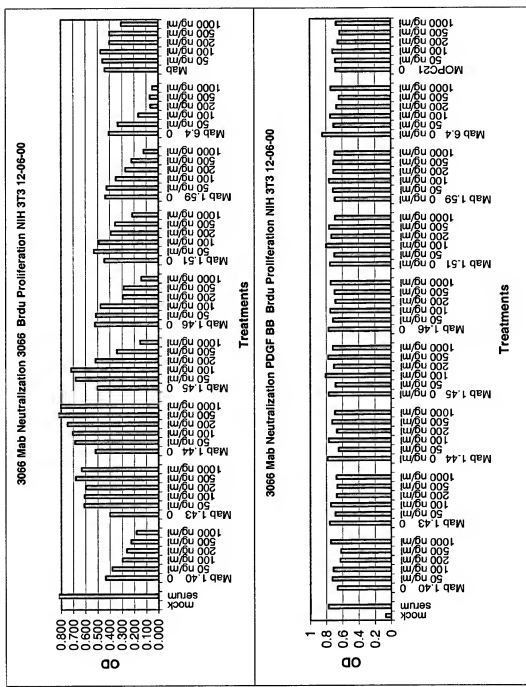


FIGURE 48

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1.19 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
6.4 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.18 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.40 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.45 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.46 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.49 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.33 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.48 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY 60
1.6 H 1 EVQLVESGGGLVPCGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.17 H 1 QVQLVESGGGLVPCGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.24 H 1 EVQLVESGGGLVPCGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.38 H 1 QVQLVESGGGLVPCGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.11 H 1 EVQLVQSGGGGLIIPGASLRLSCAASGFTVSSNYMSWVRQAPGKGLWVAVITWYDGSNKYY 59
1.23 H 1 EVQLVQSGAEVKKPGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.25 H 1 EVQLVQSGAEVKKPGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.29 H 1 EVQLVQSGAEVKKPGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.39 H 1 EVQLVQSGAEVKKPGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
1.51 H 1 EVQLVQSGAEVKKPGASLRLSCAASGFTFSYSGMHVWRQAPGKGLWVAVITWYDGSNKYY 60
      [----- CDR1 -----] [----- CDR2 -----]

1.19 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--DVM-ITFGGVIVH-YGMDEV 116
6.4 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--GFG-YSYN-YDYY-YGMDEV 115
1.18 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--EG--IAVAGTYYYYGMDEV 116
1.40 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--DIV-VVVAATNYY-NGMDEV 116
1.45 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--GSG-YSYG-YDYY-YGMDEV 115
1.46 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--DIV-VVVATDYY-YGMDEV 116
1.49 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--MRD-IVATSYYYFYGMDEV 117
1.33 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--DHY-YDSSDYLYYYGLDEV 117
1.48 H 61 AOKFQGRVTMTIRNTISISTAYMELSSLSEDPAVYYCAR--VEY-YDGSYYVYEDY--- 115
1.6 H 61 ADSVKGREFTISRDNKNTITLQMNSLRAEDPAVYYCAR--IMI---TFG-GIATSYFETW 116
1.17 H 61 ADSVKGREFTISRDNKNTITLQMNSLRAEDPAVYYCAR--QGY---RYA-GYYDYDGMDEV 116
1.24 H 61 ADSVKGREFTISRDNKNTITLQMNSLRAEDPAVYYCAR--QGY---SYG-YVYDYDGMDEV 116
1.38 H 61 ADSVKGREFTISRDNKNTITLQMNSLRAEDPAVYYCAR--GYYD--SSD-YLYYYGYDGMDEV 117
1.11 H 60 ADSVKGREFTISRDNKNTITLQMNSLRAEDPAVYYCAR--TUTT-----NYYGYDGMDEV 110
1.23 H 61 SPSPFGVYVITISADKSIISTAYLQWSLKASDTAMYYCARHVSY---YVSGSY-YNVDYV 116
1.25 H 61 SPSPFGVYVITISADKSIISTAYLQWSLKASDTAMYYCARHVSY---YVSGSY-YNVDYV 116
1.29 H 61 SPSPFGVYVITISADKSIISTAYLQWSLKASDTAMYYCARHVSY---YVSGSY-YNVDYV 116
1.39 H 61 SPSPFGVYVITISADKSIISTAYLQWSLKASDTAMYYCARHVSY---YVSGSY-YNVDYV 116
1.51 H 61 SPSPFGVYVITISADKSIISTAYLQWSLKASDTAMYYCARHVSY---YVSGSY-YNVDYV 116
      [----- CDR3 -----]

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FIGURE 48 (CONT)

1.19	H	117	GQGTIVTVSS	126
6.4	H	116	GQGTIVTVSS	125
1.18	H	117	GQGTIVTVSS	126
1.40	H	117	GQGTIVTVSS	126
1.45	H	116	GQGTIVTVSS	125
1.46	H	117	GQGTIVTVSS	126
1.49	H	118	GQGTIVTVSS	127
1.33	H	118	GQGTIVTVSS	127
1.48	H	116	GQGTIVTVSS	125
1.6	H	117	GQGTIVTVSS	126
1.17	H	117	GQGTIVTVSS	126
1.24	H	117	GQGTIVTVSS	126
1.38	H	118	GQGTIVTVSS	127
1.11	H	111	GQGTIVTVSS	120
1.23	H	117	GQGTIVTVSS	126
1.25	H	117	GQGTIVTVSS	126
1.29	H	120	GQGTIVTVSS	129
1.39	H	117	GQGTIVTVSS	126
1.51	H	117	GQGTIVTVSS	126

FIGURE 49

1.48 L 1 DIQMTQSPSSLSASVGDRTITCRASQGIS-----WLAWYQOKPGKAPKRLITYAASITLQ 55
 1.49 L 1 DIVMTQSPSLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPDLLTYLGSSRA 60
 1.11 L 1 DIVMTQSPSLSLPVTPGEPASISCRSSQSLLQSNGYNYLDWYLQKPGQSPDLLTYLGSSRA 60
 1.29 L 1 DIVMTQSPSLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPDLLTYLGSSRA 60
 1.45 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLAWYQOKPGKAPKRLITYAASITLQ 55
 1.33 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----YLAWYQOKPGKAPKRLITYAASITLQ 55
 1.38 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----YLAWYQOKPGKAPKRLITYAASITLQ 55
 6.4 L 1 DIVLTQSPCTLSLSPGEPATLSCRASQSVSSS-----YLAWYQOKPGKAPKRLITYAASITLQ 56
 1.51 L 1 DIVLTQSPCTLSLSPGEPATLSCRASQSVSSS-----YLAWYQOKPGKAPKRLITYAASITLQ 56
 1.19 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.18 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.16 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.23 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.25 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.39 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.17 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.24 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 1.46 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISN-----DLGWYQOKPGKAPKRLITYAASITLQ 55
 [-----CDR1-----] [-----CDR2-----]
 1.48 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFAVYYCQSNSEFT--FGGCTKVEIK 107
 1.49 L 61 SGVPSRFRSGSGSGTFTLTISRVEADVGWYYCQALQTLT--FGGCTKVEIK 111
 1.11 L 61 SGVPSRFRSGSGSGTFTLTISRVEADVGWYYCQALQTLT--FGGCTKVEIK 111
 1.29 L 61 SGVPSRFRSGSGSGTFTLTISRVEADVGWYYCQALQSLMCSFGGCTKVEIK 113
 1.45 L 56 LGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQKNSAPFT--FGGCTKVEIK 107
 1.33 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQKNSAPFT--FGGCTKVEIK 107
 1.38 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQKNSAPFT--FGGCTKVEIK 107
 6.4 L 57 TCHPDRFRSGSGSGTFTLTISRLEPEDFAVYYCQYGSSEPC--FGGCTKVEIK 108
 1.51 L 57 TCHPDRFRSGSGSGTFTLTISRLEPEDFAVYYCQYGSSEFT--FGGCTKVEIK 108
 1.19 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEPC--FGGCTKVEIK 107
 1.18 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.16 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.23 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.25 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.39 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.17 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.24 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 1.46 L 56 SGVPSRFRSGSGSGTFTLTISLQPEDFATYYCQHNSEFT--FGGCTKVEIK 107
 [-----CDR3-----]

FIGURE 50

1.19	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
6.4	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.18	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.40	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.45	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.46	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60
1.49	H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY	60

[____CDR1____] [____CDR2____]

1.19	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	119
6.4	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	118
1.18	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	119
1.40	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	119
1.45	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	118
1.46	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	119
1.49	H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSED	TAVYYCARDVMITFGG-VIVHYGMDVWGQG	120

[____CDR3____]

1.19	H	120	TTVTVSS	126
6.4	H	119	TTVTVSS	125
1.18	H	120	TTVTVSS	126
1.40	H	120	TTVTVSS	126
1.45	H	119	TTVTVSS	125
1.46	H	120	TTVTVSS	126
1.49	H	121	TTVTVSS	127

FIGURE 51

1.33 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
1.48 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
[____CDR1____] [____CDR2____]

1.33 H 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DHYYDS--LYYYGLDVWG 118
1.48 H 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--VEYYDS--GYYVFDY----WG 116
[____CDR3____]

1.33 H 119 QGTLVTVSS 127
1.48 H 117 QGTLVTVSS 125

1.33 H 128 QGTLVTVSS 135
1.48 H 128 QGTLVTVSS 135
1.33 H 136 QGTLVTVSS 143
1.48 H 136 QGTLVTVSS 143
1.33 H 144 QGTLVTVSS 151
1.48 H 144 QGTLVTVSS 151
1.33 H 152 QGTLVTVSS 159
1.48 H 152 QGTLVTVSS 159
1.33 H 160 QGTLVTVSS 167
1.48 H 160 QGTLVTVSS 167
1.33 H 168 QGTLVTVSS 175
1.48 H 168 QGTLVTVSS 175
1.33 H 176 QGTLVTVSS 183
1.48 H 176 QGTLVTVSS 183
1.33 H 184 QGTLVTVSS 191
1.48 H 184 QGTLVTVSS 191
1.33 H 192 QGTLVTVSS 199
1.48 H 192 QGTLVTVSS 199
1.33 H 200 QGTLVTVSS 207
1.48 H 200 QGTLVTVSS 207
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1.48 H 208 QGTLVTVSS 215
1.33 H 216 QGTLVTVSS 223
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1.33 H 248 QGTLVTVSS 255
1.48 H 248 QGTLVTVSS 255
1.33 H 256 QGTLVTVSS 263
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1.33 H 296 QGTLVTVSS 303
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1.33 H 304 QGTLVTVSS 311
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1.33 H 504 QGTLVTVSS 511
1.48 H 504 QGTLVTVSS 511
1.33 H 512 QGTLVTVSS 519
1.48 H 512 QGTLVTVSS 519
1.33 H 520 QGTLVTVSS 527
1.48 H 520 QGTLVTVSS 527
1.33 H 528 QGTLVTVSS 535
1.48 H 528 QGTLVTVSS 535
1.33 H 536 QGTLVTVSS 543
1.48 H 536 QGTLVTVSS 543
1.33 H 544 QGTLVTVSS 551
1.48 H 544 QGTLVTVSS 551
1.33 H 552 QGTLVTVSS 559
1.48 H 552 QGTLVTVSS 559
1.33 H 560 QGTLVTVSS 567
1.48 H 560 QGTLVTVSS 567
1.33 H 568 QGTLVTVSS 575
1.48 H 568 QGTLVTVSS 575
1.33 H 576 QGTLVTVSS 583
1.48 H 576 QGTLVTVSS 583
1.33 H 584 QGTLVTVSS 591
1.48 H 584 QGTLVTVSS 591
1.33 H 592 QGTLVTVSS 599
1.48 H 592 QGTLVTVSS 599
1.33 H 600 QGTLVTVSS 607
1.48 H 600 QGTLVTVSS 607
1.33 H 608 QGTLVTVSS 615
1.48 H 608 QGTLVTVSS 615
1.33 H 616 QGTLVTVSS 623
1.48 H 616 QGTLVTVSS 623
1.33 H 624 QGTLVTVSS 631
1.48 H 624 QGTLVTVSS 631
1.33 H 632 QGTLVTVSS 639
1.48 H 632 QGTLVTVSS 639
1.33 H 640 QGTLVTVSS 647
1.48 H 640 QGTLVTVSS 647
1.33 H 648 QGTLVTVSS 655
1.48 H 648 QGTLVTVSS 655
1.33 H 656 QGTLVTVSS 663
1.48 H 656 QGTLVTVSS 663
1.33 H 664 QGTLVTVSS 671
1.48 H 664 QGTLVTVSS 671
1.33 H 672 QGTLVTVSS 679
1.48 H 672 QGTLVTVSS 679
1.33 H 680 QGTLVTVSS 687
1.48 H 680 QGTLVTVSS 687
1.33 H 688 QGTLVTVSS 695
1.48 H 688 QGTLVTVSS 695
1.33 H 696 QGTLVTVSS 703
1.48 H 696 QGTLVTVSS 703
1.33 H 704 QGTLVTVSS 711
1.48 H 704 QGTLVTVSS 711
1.33 H 712 QGTLVTVSS 719
1.48 H 712 QGTLVTVSS 719
1.33 H 720 QGTLVTVSS 727
1.48 H 720 QGTLVTVSS 727
1.33 H 728 QGTLVTVSS 735
1.48 H 728 QGTLVTVSS 735
1.33 H 736 QGTLVTVSS 743
1.48 H 736 QGTLVTVSS 743
1.33 H 744 QGTLVTVSS 751
1.48 H 744 QGTLVTVSS 751
1.33 H 752 QGTLVTVSS 759
1.48 H 752 QGTLVTVSS 759
1.33 H 760 QGTLVTVSS 767
1.48 H 760 QGTLVTVSS 767
1.33 H 768 QGTLVTVSS 775
1.48 H 768 QGTLVTVSS 775
1.33 H 776 QGTLVTVSS 783
1.48 H 776 QGTLVTVSS 783
1.33 H 784 QGTLVTVSS 791
1.48 H 784 QGTLVTVSS 791
1.33 H 792 QGTLVTVSS 799
1.48 H 792 QGTLVTVSS 799
1.33 H 800 QGTLVTVSS 807
1.48 H 800 QGTLVTVSS 807
1.33 H 808 QGTLVTVSS 815
1.48 H 808 QGTLVTVSS 815
1.33 H 816 QGTLVTVSS 823
1.48 H 816 QGTLVTVSS 823
1.33 H 824 QGTLVTVSS 831
1.48 H 824 QGTLVTVSS 831
1.33 H 832 QGTLVTVSS 839
1.48 H 832 QGTLVTVSS 839
1.33 H 840 QGTLVTVSS 847
1.48 H 840 QGTLVTVSS 847
1.33 H 848 QGTLVTVSS 855
1.48 H 848 QGTLVTVSS 855
1.33 H 856 QGTLVTVSS 863
1.48 H 856 QGTLVTVSS 863
1.33 H 864 QGTLVTVSS 871
1.48 H 864 QGTLVTVSS 871
1.33 H 872 QGTLVTVSS 879
1.48 H 872 QGTLVTVSS 879
1.33 H 880 QGTLVTVSS 887
1.48 H 880 QGTLVTVSS 887
1.33 H 888 QGTLVTVSS 895
1.48 H 888 QGTLVTVSS 895
1.33 H 896 QGTLVTVSS 903
1.48 H 896 QGTLVTVSS 903
1.33 H 904 QGTLVTVSS 911
1.48 H 904 QGTLVTVSS 911
1.33 H 912 QGTLVTVSS 919
1.48 H 912 QGTLVTVSS 919
1.33 H 920 QGTLVTVSS 927
1.48 H 920 QGTLVTVSS 927
1.33 H 928 QGTLVTVSS 935
1.48 H 928 QGTLVTVSS 935
1.33 H 936 QGTLVTVSS 943
1.48 H 936 QGTLVTVSS 943
1.33 H 944 QGTLVTVSS 951
1.48 H 944 QGTLVTVSS 951
1.33 H 952 QGTLVTVSS 959
1.48 H 952 QGTLVTVSS 959
1.33 H 960 QGTLVTVSS 967
1.48 H 960 QGTLVTVSS 967
1.33 H 968 QGTLVTVSS 975
1.48 H 968 QGTLVTVSS 975
1.33 H 976 QGTLVTVSS 983
1.48 H 976 QGTLVTVSS 983
1.33 H 984 QGTLVTVSS 991
1.48 H 984 QGTLVTVSS 991
1.33 H 992 QGTLVTVSS 999
1.48 H 992 QGTLVTVSS 999
1.33 H 1000 QGTLVTVSS 1007
1.48 H 1000 QGTLVTVSS 1007

FIGURE 52

1.17 H 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYSGMHVVRQAPGKGLEWVAIIWYDGSNKYY 60
 1.24 H 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYSGMHVVRQAPGKGLEWVAIIWYDGSNKYY 60
 1.38 H 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYSGMHVVRQAPGKGLEWVAIIWYDGSNKYY 60
 [____CDR1____] [____CDR2____]

1.17 H 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY- RYAGY YDYGM DVWGQG 119
 1.24 H 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY- SYGYV YDYGM DVWGQG 119
 1.38 H 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY- YDSSDYLY YDYGM DVWGQG 120
 [_____] [____CDR3____]

1.17 H 120 TTVTVSS 126
 1.24 H 120 TTVTVSS 126
 1.38 H 121 TTVTVSS 127

1.17 H 120 TTVTVSS 126
 1.24 H 120 TTVTVSS 126
 1.38 H 121 TTVTVSS 127

FIGURE 53

1.23	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS	TRY	60
1.25	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS	TRY	60
1.29	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS	TRY	60
1.39	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS	TRY	60
1.51	H	1	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS	TRY	60
			{ CDR1 }	{ CDR2 }	
1.23	H	61	SPSFQGOVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYVSG---	SYNVFDW	117
1.25	H	61	SPSFQGOVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYVSG---	SYNVFDW	117
1.29	H	61	SPSFQGOVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYVSG---	SYNVFDW	120
1.39	H	61	SPSFQGOVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYVSG---	SYNVFDW	117
1.51	H	61	SPSFQGOVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYVSG---	SYNVFDW	117
			{ CDR3 }		
1.23	H	118	QGTLLTVSS	126	
1.25	H	118	QGTLLTVSS	126	
1.29	H	121	QGTLLTVSS	129	
1.39	H	118	QGTLLTVSS	126	
1.51	H	118	QGTLLTVSS	126	
1.23	H	118	QGTLLTVSS	126	
1.25	H	118	QGTLLTVSS	126	
1.29	H	121	QGTLLTVSS	129	
1.39	H	118	QGTLLTVSS	126	
1.51	H	118	QGTLLTVSS	126	


$$\begin{array}{ccccccc} \text{number of} & \text{number of} & \text{number of} & \text{number of} & \text{number of} & \text{number of} & \text{number of} \\ \text{nodes} & \text{edges} & \text{nodes} & \text{edges} & \text{nodes} & \text{edges} & \text{nodes} \\ \hline 1 & 0 & 1 & 0 & 1 & 0 & 1 \\ 2 & 1 & 2 & 2 & 2 & 2 & 2 \\ 3 & 3 & 3 & 6 & 3 & 6 & 3 \\ 4 & 6 & 4 & 12 & 4 & 12 & 4 \\ 5 & 10 & 5 & 20 & 5 & 20 & 5 \\ 6 & 15 & 6 & 30 & 6 & 30 & 6 \\ 7 & 21 & 7 & 42 & 7 & 42 & 7 \\ 8 & 28 & 8 & 56 & 8 & 56 & 8 \\ 9 & 36 & 9 & 72 & 9 & 72 & 9 \\ 10 & 45 & 10 & 90 & 10 & 90 & 10 \end{array}$$

FIGURE 55

1.45 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISNQLAWYQQKPGKVPRLIIYAASTLQLGVP 60
1.33 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISNQLAWYQQKPGKVPRLIIYAASTLQSGVPS 60
1.38 L 1 DIQMTQSPSSLSASVGDRTITCRASQGISNQLAWYQQKPGKVPRLIIYAASTLQSGVPS 60
[_CDR1_] [_CDR2_]

1.45 L 61 RFSGSGSGTDFTLTISSLQPEDVAHYCYCKNSAPFTFGSGTKVEIK 107
1.33 L 61 RFSGSGSGTDFTLTISSLQPEDVAHYCYCKNSAPFTFGSGTKVEIK 107
1.38 L 61 RFSGSGSGTDFTLTISSLQPEDVAHYCYCKNSAPFTFGSGTKVEIK 107
[_CDR3_]

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FIGURE 56

6.4 L	1	EIVLTQSPGTL SLSPGERATL SCRASQSVSSSYLAWYQOKPGQAPRLLIYAT SSRATGIP	60
1.51 L	1	EIVLTQSPGTL SLSPGERATL SCRASQSVSSSYLAWYQOKPGQAPRLLIY GASNRATGIP	60
		[<u>CDR1</u>]	[<u>CDR2</u>]
6.4 L	61	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPC SG Q G T K L E T K	108
1.51 L	61	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS LF T E G P G T K V D I K	108
		[<u>CDR3</u>]	

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FIGURE 57

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1.19 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.18 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.16 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.23 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.25 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.39 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.17 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.24 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
1.46 L 1 DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60

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[____CDR1____]

[____CDR2____]

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1.19 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPFTFGSGTKVEIK 107
1.18 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPFTFGSGTKVDIK 107
1.16 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSVPLTFGGGTKVEIK 107
1.23 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK 107
1.25 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK 107
1.39 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK 107
1.17 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSVPLTFGGGTKVEIK 107
1.24 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSVPLTFGGGTKVEIK 107
1.46 L 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGTKVEIK 107

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[____CDR3____]